



Title: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR  
IMPAIRED GLUCOSE TOLERANCE CONDITIONS  
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Comparison of the human AKT protein sequence to the cosmid sequence C12D8, located in the genetic interval where sup(mg144) maps. Numbering in the AKT protein sequence by amino acid residues, and in the cosmid sequence by nucleotide position.

Score = 450 (207.4 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165  
Identities = 79/121 (65%), Positives = 97/121 (80%), Frame = +1

SEQ ID No: 87 Query: 319 EVLEDNDYGRAVDWWGLGVVMYEMMCGRLPFYQNQDHEKLFELILMEEIRFPRTLGPEAKS 378  
SEQ ID No: 325 +VL+D+DYGR VDWG+GVVMYEMMCGRLPFY++DH KLFELI+ ++RFP L EA++  
SEQ ID No: 88 Sbjct: 33685 QVLDDHDYGRCPWDWVGVVVYEMMCGRLPFYSKDHNLFLFELIMAGDLRFPSKLSQEART 33864

Query: 379 LLSGLLKKDPQTQLGGGSEDAKEIMQHRRFPANIVWQDVYEKKLSPPFKPQVTSETDTRYFD 439  
LL+GLL KDPTQRLGGG EDA EI + FF + W+ Y K++ PP+KP V SETDT YFD  
Sbjct: 33865 LLTGLLVKDPTQRLGGGPEDALEICRADPFPRTVDWEATYRKEIEPPYKPNVQSETDTSYFD 34047

Score = 256 (118.0 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165  
Identities = 48/66 (72%), Positives = 59/66 (89%), Frame = +1

SEQ ID No: 89 Query: 146 TMNEFEYLKLLGKGTFGKVILVKEKATGRYYAMKILKKEVIVAKDEVARTLTERVLQNS 205  
SEQ ID No: 326 TM +F++LK+LGKGTFGKVIL KEK T + YA+KILKK+VI+A++EVARTLTERVLQ  
SEQ ID No: 90 Sbjct: 32314 TMEDPDFLKVLGKGTFGKVILCKEKTQKLYAIKILKKDVIAREEEVAHTLTERVLQRC 32493

Query: 206 RHPFLT 211  
+HPFLT  
Sbjct: 32494 KHPFLT 32511

Score = 190 (87.6 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165  
Identities = 36/45 (80%), Positives = 37/45 (82%), Frame = +2

SEQ ID No: 91 Query: 276 KLENLMLDKDGHIKITDFGLCKEGIKDGATMKTFCGTPPEYLAPEV 320  
KLENL+LDKGHIKI DFGLCKE I G TFCGTPEYLAPEV  
SEQ ID No: 99 Sbjct: 33509 KLENLLDKDGHIKIADFGLCKEISPGDKTSTFCGTPEYLAPEV 33643

Score = 188 (86.7 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165  
Identities = 37/57 (64%), Positives = 42/57 (73%), Frame = +3

SEQ ID No: 93 Query: 209 FLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAEVSAALYHL 265  
SEQ ID No: 100 + LKYSFQ LCFVM++ANGGEL H+ + FSE RARFYGAEV AL YLH  
SEQ ID No: 94 Sbjct: 32667 YFQELKYSFQEQHYLCFVMQFANGGELFTHVRKGTFSEPRARFYGAEVLAALGYHL 32837

Score = 166 (76.5 bits), Expect = 5.2e-165, Sum P(7) = 5.2e-165  
Identities = 29/59 (49%), Positives = 42/59 (71%), Frame = +1

SEQ ID No: 95 Query: 53 NNFSVAQCQLMKTERPRPNTFIIRCLQWTTVIERTFHVTPEEREEWATAIQTVADGLK 111  
+ F++ Q M E+PRPN F++RCLQWTTVIERTF+ E+ E R+ W AI++++ K  
SEQ ID No: 101 Sbjct: 31846 STFAIFYFQTMLFEKPRPNMFVRCLQWTTVIERTFYAESAEVRQRWIHAIESISKYK 32022

Score = 134 (61.8 bits), Expect = 5.2e-167, Sum P(8) = 5.2e-167  
Identities = 24/33 (72%), Positives = 30/33 (90%), Frame = +3

SEQ ID No: 97 Query: 210 LTALKYSFQTHDRLCFVMEYANGGELFFHLSRE 242  
SEQ ID No: 102 L LKYSFQT+DRLCFVME+A GG+L++HL+RE  
SEQ ID No: 98 Sbjct: 33156 LQELKYSFQTNDRLCFVMEFAIGGDLYYHNLRE 33254

Fig. 25